SEQUENCE LISTING

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<110>  SYRRX, INC.

<120>  HISTONE DEACETYLASE INHIBITORS

<130>  SYR-HDAC-5002-U

<140>  Not Yet Assigned
<141>  2003-10-07

<150>  60/417,238
<151>  2002-10-08

<160>  3

<170>  PatentIn version 3.1

<210>  1
<211>  377
<212>  PRT
<213>  Homo sapiens

<220>
<221>  Amino acid sequence for full length human wild type HDAC8
<222>  (1)..(377)
<223>

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<308>  Genbank Accession Number NP_060956
<309>  2001-02-26
<313>  (1)..(377)

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Met Glu Glu Pro Glu Glu Pro Ala Asp Ser Gly Gln Ser Leu Val Pro
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Val Tyr Ile Tyr Ser Pro Glu Tyr Val Ser Met Cys Asp Ser Leu Ala
            20                  25                  30


Lys Ile Pro Lys Arg Ala Ser Met Val His Ser Leu Ile Glu Ala Tyr
        35                  40                  45


Ala Leu His Lys Gln Met Arg Ile Val Lys Pro Lys Val Ala Ser Met
    50                  55                  60


Glu Glu Met Ala Thr Phe His Thr Asp Ala Tyr Leu Gln His Leu Gln
65                  70                  75                  80


Lys Val Ser Gln Glu Gly Asp Asp Asp His Pro Asp Ser Ile Glu Tyr
                85                  90                  95


Gly Leu Gly Tyr Asp Cys Pro Ala Thr Glu Gly Ile Phe Asp Tyr Ala
            100                 105                 110
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Ala Ala Ile Gly Gly Ala Thr Ile Thr Ala Ala Gln Cys Leu Ile Asp
        115                 120                 125

Gly Met Cys Lys Val Ala Ile Asn Trp Ser Gly Gly Trp His His Ala
    130                 135                 140

Lys Lys Asp Glu Ala Ser Gly Phe Cys Tyr Leu Asn Asp Ala Val Leu
145                 150                 155                 160

Gly Ile Leu Arg Leu Arg Arg Lys Phe Glu Arg Ile Leu Tyr Val Asp
                165                 170                 175

Leu Asp Leu His His Gly Asp Gly Val Glu Asp Ala Phe Ser Phe Thr
            180                 185                 190

Ser Lys Val Met Thr Val Ser Leu His Lys Phe Ser Pro Gly Phe Phe
        195                 200                 205

Pro Gly Thr Gly Asp Val Ser Asp Val Gly Leu Gly Lys Gly Trp Tyr
    210                 215                 220

Tyr Ser Val Asn Val Pro Ile Gln Asp Gly Ile Gln Asp Glu Lys Tyr
225                 230                 235                 240

Tyr Gln Ile Cys Glu Ser Val Leu Lys Glu Val Tyr Gln Ala Phe Asn
                245                 250                 255

Pro Lys Ala Val Val Leu Gln Leu Gly Ala Asp Thr Ile Ala Gly Asp
            260                 265                 270

Pro Met Cys Ser Phe Asn Met Thr Pro Val Gly Ile Gly Lys Cys Leu
        275                 280                 285

Lys Tyr Ile Leu Gln Trp Gln Leu Ala Thr Leu Ile Leu Gly Gly Gly
    290                 295                 300

Gly Tyr Asn Leu Ala Asn Thr Ala Arg Cys Trp Thr Tyr Leu Thr Gly
305                 310                 315                 320

Val Ile Leu Gly Lys Thr Leu Ser Ser Glu Ile Pro Asp His Glu Phe
                325                 330                 335

Phe Thr Ala Tyr Gly Pro Asp Tyr Val Leu Glu Ile Thr Pro Ser Cys
            340                 345                 350

Arg Pro Asp Arg Asn Glu Pro His Arg Ile Gln Gln Ile Leu Asn Tyr
        355                 360                 365
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Ile Lys Gly Asn Leu Lys His Val Val
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<210> 2
<211> 1134
<212> DNA
<213> Homo sapiens

<220>
<221> Human cDNA sequence encoding residues 1-377 of HDAC8
<222> (1)..(1134)
<223>

<300>
<308> Genbank Accession Number NM_018486
<309> 2001-02-26
<313> (1)..(1134)

<400> 2

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gtgcattctt tgattgaagc atatgcactg cataagcaga tgaggatagt taagcctaaa     180

gtggcctcca tggaggagat ggccaccttc cacactgatg cttatctgca gcatctccag     240

aaggtcagcc aagagggcga tgatgatcat ccggactcca tagaatatgg gctaggttat     300

gactgcccag ccactgaagg gatatttgac tatgcagcag ctataggagg ggctacgatc     360

acagctgccc aatgcctgat tgacggaatg tgcaaagtag caattaactg gtctggaggg     420

tggcatcatg caaagaaaga tgaagcatct ggtttttgtt atctcaatga tgctgtcctg     480

ggaatattac gattgcgacg gaaatttgag cgtattctct acgtggattt ggatctgcac     540

catggagatg gtgtagaaga cgcattcagt ttcacctcca aagtcatgac cgtgtccctg     600

cacaaattct ccccaggatt tttcccagga acaggtgacg tgtctgatgt tggcctaggg     660

aagggatggt actacagtgt aaatgtgccc attcaggatg gcatacaaga tgaaaaatat     720

taccagatct gtgaaagcgt actaaaggaa gtataccaag cctttaatcc caaagcagtg     780

gtcttacagc tgggagctga cacaatagct ggggatccca tgtgctcctt taacatgact     840

ccagtgggaa ttggcaagtg tcttaagtac atccttcaat ggcagttggc aacactcatt     900

ttgggaggag gaggctataa ccttgccaac acggctcgat gctggacata cttgaccggg     960

gtcatcctag ggaaaacact atcctctgag atcccagatc atgagttttt cacagcatat    1020

ggtcctgatt atgtgctgga aatcacgcca agctgccggc cagaccgcaa tgagccccac    1080

cgaatccaac aaatcctcaa ctacatcaaa gggaatctga agcatgtggt ctag          1134
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<210> 3
<211> 385
<212> PRT

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<213>  Homo sapiens

<220>
<221>  Amino acid sequence for residues 1-377 of HDAC8 with a cleavable N-terminal
6x-histidine tag
<222>  (1)..(385)
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<220>
<221>  Cleavable N-terminal 6x-histidine tag
<222>  (1)..(8)
<223>

<400>  3

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1               5                   10                  15


Asp Ser Gly Gln Ser Leu Val Pro Val Tyr Ile Tyr Ser Pro Glu Tyr
                20                  25                  30


Val Ser Met Cys Asp Ser Leu Ala Lys Ile Pro Lys Arg Ala Ser Met
            35                  40                  45


Val His Ser Leu Ile Glu Ala Tyr Ala Leu His Lys Gln Met Arg Ile
        50                  55                  60


Val Lys Pro Lys Val Ala Ser Met Glu Glu Met Ala Ala Phe His Thr
65                  70                  75                  80


Asp Ala Tyr Leu Gln His Leu Gln Lys Val Ser Gln Glu Gly Asp Asp
                85                  90                  95


Asp His Pro Asp Ser Ile Glu Tyr Gly Leu Gly Tyr Asp Cys Pro Ala
            100                 105                 110


Thr Glu Gly Ile Phe Asp Tyr Ala Ala Ala Ile Gly Gly Ala Thr Ile
        115                 120                 125


Thr Ala Ala Gln Cys Leu Ile Asp Gly Met Cys Lys Val Ala Ile Asn
    130                 135                 140


Trp Ser Gly Gly Trp His His Ala Lys Lys Asp Glu Ala Ser Gly Phe
145                 150                 155                 160


Cys Tyr Leu Asn Asp Ala Val Leu Gly Ile Leu Arg Leu Arg Arg Lys
                165                 170                 175


Phe Glu Arg Ile Leu Tyr Val Asp Leu Asp Leu His His Gly Asp Gly
            180                 185                 190
```

```
Val Glu Asp Ala Phe Ser Phe Thr Ser Lys Val Met Thr Val Ser Leu
        195                 200                 205

His Lys Phe Ser Pro Gly Phe Phe Pro Gly Thr Gly Asp Val Ser Asp
    210                 215                 220

Val Gly Leu Gly Lys Gly Arg Tyr Tyr Ser Val Asn Val Pro Ile Gln
225                 230                 235                 240

Asp Gly Ile Gln Asp Glu Lys Tyr Tyr Gln Ile Cys Glu Ser Val Leu
                245                 250                 255

Lys Glu Val Tyr Gln Ala Phe Asn Pro Lys Ala Val Val Leu Gln Leu
            260                 265                 270

Gly Ala Asp Thr Ile Ala Gly Asp Pro Met Cys Ser Phe Asn Met Thr
        275                 280                 285

Pro Val Gly Ile Gly Lys Cys Leu Lys Tyr Ile Leu Gln Trp Gln Leu
    290                 295                 300

Ala Thr Leu Ile Leu Gly Gly Gly Gly Tyr Asn Leu Ala Asn Thr Ala
305                 310                 315                 320

Arg Cys Trp Thr Tyr Leu Thr Gly Val Ile Leu Gly Lys Thr Leu Ser
                325                 330                 335

Ser Glu Ile Pro Asp His Glu Phe Phe Thr Ala Tyr Gly Pro Asp Tyr
            340                 345                 350

Val Leu Glu Ile Thr Pro Ser Cys Arg Pro Asp Arg Asn Glu Pro His
        355                 360                 365

Arg Ile Gln Gln Ile Leu Asn Tyr Ile Lys Gly Asn Leu Lys His Val
    370                 375                 380

Val
385
```